

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2003, 09:48:28 ; Search time 9333.87 seconds

(without alignments)
1181.073 Million cell updates/sec

Title: US-09-922-895-3

Perfect score: 3586

Sequence: 1 GGATCCCTACCTTCCCATC.....CTATCAGGAGAGACTGAA 3586

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vl:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

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34: em_htg_pln:*

35: em_htg_rod:*

36: em_htg_mam:*

37: em_htg_vtl:*

38: em_sy:*

39: em_htgo_hum:*

40: em_htgo_mus:*

41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	3586	100.0	3586	6	AX030930
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4	3492.8	97.4	197279	9	AC104439
5	3481.6	97.1	220965	2	HSA13268
6	3408.6	95.1	7010	9	AF224496S2
7	3388	94.5	3388	9	AF237380S2
8	2406	67.1	7201	6	AX345239
9	2271.8	63.4	7201	6	AX345238
10	1066.2	29.7	1310	6	AF262300
11	358.6	10.0	436	9	AF262304
12	344.2	9.6	1915	6	BD006761
13	219.8	6.1	112967	9	AC025177
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37	212.6	5.9	145656	9	HS11K10
38	212.6	5.9	340000	9	HS21C009
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45	212.2	5.9	224931	9	AC008540

ALIGNMENTS

RESULT 1

LOCUS AR164120

DEFINITION Sequence 3 from patent US 6271347.

ACCESSION AR164120

VERSION AR164120.1 GI:16235066

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 3586)

AUTHORS Daugherty,B.L., Demartino,J.A., Siciliano,S.J. and Springer,M.S.

TITLE Eosinophil eotaxin receptor

JOURNAL Patent: US 6271347-A 3 07-AUG-2001;

FEATURES Location/Qualifiers

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source 1. .3586 /organism="unknown"
BASE COUNT 1003 a 784 c 701 g 1098 t
ORIGIN
Query Match 100.0%; Score 3586; DB 6; Length 3586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGATCCCTACCTTCCCATGAGCTAGGGGGCATGGAGGCGCTCTGCTAGATGGGA 60

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RESULT 2
AX030930 3586 bp DNA linear PAT 20-SEP-2000
LOCUS Sequence 3 from Patent EP1012190.
DEFINITION AX030930
ACCESSION AX030930
VERSION AX030930.1 GI:10278335
KEYWORDS
SOURCE
ORGANISM
unidentified.
unidentified.
REFERENCE
1 (bases 1 to 3586)
AUTHORS Daugherty, B.L., Demartino, J.A., Siciliano, S.J. and Springer, M.S.
TITLE Eosinophil eotaxin receptor
JOURNAL Patent: EP 1012190-A 3 28-JUN-2000;
MERCK & CO INC (US)
FEATURES
location/Qualifiers
source 1..3586
BASE COUNT 1003 a 784 c 701 g 1098 t
ORIGIN
Query Match 100.0%; Score 3586; DB 6; Length 3586;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3586; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 181 GTTCATGGCATGGGAGAGGAGTCAAGAGACAGAGCTTGCCATGCTTACCATGCA 240
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Db 181 GTTCATGGCATGGGAGAGGAGTCAAGAGACAGAGCTTGCCATGCTTACCATGCA 240
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OY	301	GAGGGCTCTCCATTCCTCAGGCCCAAGAAAGCATAGTAAGTAATCTCATAGATATTAGC	360
Db	301	GAGGGCTCTCCATTCCTCAGGCCCAAGAAAGCATAGTAAGTAATCTCATAGATATTATAGC	360
OY	361	TACAAACCCACACAGCAGGTTCCAGAAAAAGGCTCAGCCTTGGAAACAGATGACCCCCAC	420
Db	361	TACAAACCCACACAGCAGGTTCCAGAAAAAGGCTCAGCCTTGGAAACAGATGACCCCCAC	420
OY	421	TCAGCAGACACCACTCATATTAATTCAGAGACCAACAGAGAGAAAGAACACCCCTTCCCA	480
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OY	481	CTTCGCCCATGTCTCAAGTTGTAGTGGCCCTTCCTCCAGATCTCTGCACATCTTGA	540
Db	481	CTTCGCCCATGTCTCAAGTTGTAGTGGCCCTTCCTCCAGATCTCTGCACATCTTGA	540
OY	541	AAGGACACTGGAAGAGAAAAGTGAATTAAGCTGACAGCATTAAGAGATGAGTAA	600
Db	541	AAGGACACTGGAAGAGAAAAGTGAATTAAGCTGACAGCATTAAGAGATGAGTAA	600
OY	601	ACCTAAATTCATTTGTCCACATGAAATGAAATCAGAGCATTAAGAGATGAGTAA	660
Db	601	ACCTAAATTCATTTGTCCACATGAAATGAAATCAGAGCATTAAGAGATGAGTAA	660
OY	661	TGTGTGAATCCTTTTTCCTCTCATCCAGCAGATGAGAAACCTGGTAAACAGACCAATA	720
Db	661	TGTGTGAATCCTTTTTCCTCTCATCCAGCAGATGAGAAACCTGGTAAACAGACCAATA	720
OY	721	GTTTGGAGACTAAAGAAATCAATTCACATTTCACTGCTGAGTTGTATGTGAGTAATTTA	780
Db	721	GTTTGGAGACTAAAGAAATCAATTCACATTTCACTGCTGAGTTGTATGTGAGTAATTTA	780
OY	781	GTTGGACCTCACTTTGTAATCTTGACACACGGGGCAATCCAAATATCGACACAAGAGATG	840
Db	781	GTTGGACCTCACTTTGTAATCTTGACACACGGGGCAATCCAAATATCGACACAAGAGATG	840
OY	841	TTAACCACTGTAATATCTCATGAGAGATTTGGGATTTTACTTTTCGTTTGTGCT	900
Db	841	TTAACCACTGTAATATCTCATGAGAGATTTGGGATTTTACTTTTCGTTTGTGCT	900
OY	901	CTTCTTCTATTTGTCTTACTTATTTAGATTAACCTATGCTTTTCCGAAAATGTAA	960
Db	901	CTTCTTCTATTTGTCTTACTTATTTAGATTAACCTATGCTTTTCCGAAAATGTAA	960
OY	961	GSCCACTTTGSAACCCATTCGAACCTCTTCACATTTTGTATCTAGATATTCACCTG	1020
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Db	1021	ATTGAGACTGGGTGAGACAGGTGAAGAACATATAGSTTTTAATTTTAAATTTTAAAT	1080
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Db	1081	ATTATTTATTTATTTATTTTGTGAGATGAGTCTGGCTGTGCCCAGGCTGAGTGCAG	1140
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Db	1141	CGCGCTGATTCACACTGTACATGACGACCTCAACCTTTCAGGCTCAAGGATTTCTCCACTC	1200
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Db	1201	AGCCCCCACTAGTTGGGACCAACAGTATGGCCCAACATGCTGGCTGAATTTCTTATTT	1260
OY	1261	TTTTGTAGAGATAGATCTCATATATTTGCCAGGCTGTGTTGAAATTCCTGGGCTCAGG	1320
Db	1261	TTTTGTAGAGATAGATCTCATATATTTGCCAGGCTGTGTTGAAATTCCTGGGCTCAGG	1320
OY	1321	TGAGCTCCACCTGGGCTCTCCAAAGACTGTGGATTAACAGGCATGAGCAAGTCCCT	1380

Db	1321	TCAGCTCTCCACCTGGGGCTCCCAAAATACATGGGATTAAGGCATGAGCAAGGTCCTT	1380
Qy	1381	GGCCCATATGAGATTTTGTCTCTCGATGCCATTCAGCTAGTATCAAGACTTGGCTCT	1440
Db	1381	GCCCATATGAGATTTTCTGTCTCTGATCCCATCAGCTAGTATCAAGACTTGGCTCT	1440
Qy	1441	GACTCTGGAGGACCTGCATCTTTCTTGACCTGTGACTTCAGTCTTAAAGCTCATAGG	1500
Db	1441	GACTCTGGAGGACCTGCATCTTTCTTGACCTGTGAACTTCAGTCTTAAAGCTCATAGG	1500
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Db	2101	CACCTTCATTTTCTCATCAACACCCCAAGTAGACCAATGGTCTCACTTTGATATATA	2160
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LOCUS Homo sapiens CC chemokine receptor 3 (CCR3) gene, complete cds.
DEFINITION AF247361
ACCESSION AF247361.1 GI:19110542
VERSION AF247361.1
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 5791)
AUTHORS Vijn,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence for a Rare TATA-less Promoter Structure Conserved between Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287

REFERENCE 2 (bases 1 to 5791)
AUTHORS Vijn,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
TITLE Direct Submission
JOURNAL Submitted (21-MAR-2000) Dept. of Mol. Diag. and Pathogenesis, U.S. Military HIV Research Program, 1600 E. Gude Drive, Rockville, MD 20850, USA

FEATURES
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polyA_site
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ORIGIN

Query Match 97.4%; Score 3494.4; DB 9; Length 5791;
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Matches 3569; Conservative 0; Mismatches 11; Indels 8; Gaps 6;

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 Db 3727 TTTCAGAAATCTGTATCCCATTTCTTCACACACACCCACAAACATTTCTGCTTTTTC 3786
 Oy 3360 CATGCC -GGTCACTGCTTAACATTGAAAGCTTCAGCTCTTTCTCTCAATCTTCTCTG 3418
 Db 3787 CATGCCGGGTCAATGCTTAACATTGAAAGCTTCAGCTCTTTCTCTCAATCTTCTCTG 3846
 Oy 3419 GCACCTGATATGCTCTTTTGAATTCATGTTAAAGAAATCCCTAGCGCTTCACATGT 3478
 Db 3847 GCACCTGATATGCTCTTTTGAATTCATGTTAAAGAAATCCCTAGCGCTTCACATGT 3906
 Oy 3479 GGCATCTTTGTTGAGTACATGAATTAATCACTGCTGTTTTCAGAAAGATGATTTATGC 3538
 Db 3907 GGCATCTTTGTTGAGTACATGAATTAATCACTGCTGTTTTCAGAAAGATGATTTATGC 3966
 Oy 3539 TTCAATTTGGGATTTGATTTTCTTCTTCTATCAACAGGAGAGTGA 3586
 Db 3967 TTCAATTTGGGATTTGATTTTCTTCTTCTATCAACAGGAGAGTGA 4014

RESULT 4
 AC104439
 LOCUS
 DEFINITION Homo sapiens chromosome 3 clone RP11-793E15, complete sequence.
 AC104439 AC024739
 VERSION
 KEYWORDS HTG.
 SOURCE
 ORGANISM human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
 Saenphumachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
 and Haugen, E.D.
 Direct Submission
 2 (bases 1 to 197279)
 Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.
 TITLE JOURNAL
 REFERENCE
 AUTHORS
 TITLE JOURNAL
 REFERENCE
 AUTHORS
 COMMENT

JOURNAL
 Submitted (11-DEC-2001) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 3 (bases 1 to 197279)
 Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,
 Saenphumachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C.
 and Haugen, E.D.
 Direct Submission
 Submitted (20-JUN-2002) Genome Center, University of Washington,
 Box 352145, Seattle, WA 98195, USA
 On Jun 20, 2002 this sequence version replaced gi:17488621.
 ----- Genome Center
 Center: University of Washington Genome Center
 Center Code: UWGC
 Web site: http://www.genome.washington.edu
 Contact: uwgchgs@u.washington.edu
 Drafting Center: WUGSC
 ----- Project Information
 Center project name: chr3
 Center clone name: RP11-793E15 (bc0564)
 ----- Summary Statistics
 Sequencing vector: unknown: 52% of reads
 Sequencing vector: plasmid: L08752: 48% of reads
 Chemistry: Dye-terminator ET: 94% of reads
 Chemistry: Dye-terminator Big Dye: 6% of reads
 Assembly program: Phrap: version 0.990319
 Consensus quality: 197168 bases at least Q40
 Consensus quality: 197255 bases at least Q30

Consensus quality: 197275 bases at least Q20
Insert size: 197279; sum-of-contigs
Quality coverage: 8.2x in Q20 bases; sum-of-contigs

Overlapping Sequences:

5': RP11-91E8 (UMGC:bc0216) AC026349
3': CTD-2565A18 (UMGC:bc0730)

Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

HindIII

BglII

EcoRI

SeqDerMap	FngPrnt	SeqDerMap	FngPrnt	SeqDerMap	FngPrnt
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2687	2617	8949	8586	8696	8661
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6382	6410	2067	2160	6	<800
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512	<800	7846	7940	2742	2803
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449	<800	3734	3895	5376	5324
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2602	2763	1334	1301	1493	1478
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2590	2617	2287	2309	823	835
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8313	8291	1814	1918	1962	2002
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1711	1683	691	<800	2900	2954
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9821	9472	5477	5348	1484	1478
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516	<800	305	<800	1005	995
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8587	8291	25245	25541	1181	1171
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7446	7581	3988	4121	18560	19002
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2088	2075	1633	1598	3603	3579
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2509	2617	631	<800	4943	5076
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3519	3501	90	<800	3239	3241
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26	<800	402	<800	953	995
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925	933	3350	3490	1621	1615
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98	<800	4577	4515	6827	6900
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6409	6410	1229	1183	79	<800
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1383	1376	4221	4331	16418	16263
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16048	15829	3980	4121	3361	3241
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1876	1877	2548	2497	872	881
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4169	4068	674	<800	4220	4193
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1674	1683	2332	2309	2848	2803
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52	<800	11445	11045	2283	2318
-----	-----	-----	-----	-----	-----
5227	5082	5692	5632	3211	3241
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15464	15829	1385	1414	4615	4632
-----	-----	-----	-----	-----	-----
14333	14296	608	<800	6823	6900
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1026	1026	3930	3895	886	881
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645	<800	1465	1414	2032	2002
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6621	6410	2382	2497	8680	8661
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8413	8291	747	<800	5163	5076
-----	-----	-----	-----	-----	-----
1401	1376	1951	2012	1547	1478
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1512	1471	642	<800	7058	6900
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5801	5644	21060	21003	1647	1615
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3256	3278	3700	3666	2753	2803
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3448	3501	1321	1301	162	<800
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2738	2763	10705	10502	1078	1093
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237	<800	3128	3317	2156	2173
-----	-----	-----	-----	-----	-----
6715	6823	183	<800	5077	5076
-----	-----	-----	-----	-----	-----
201	<800	3255	3490	154	<800
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1002	1026	5693	5632	1571	1478
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221	<800	3380	3317	219	<800
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2854	2899	237	<800	520	<800
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6998	7317	431	<800	1540	1478
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1174	1145	2152	2160	1479	1478
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7876	8291	249	<800	1613	1615
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1911	1877	2599	2778	1399	1478
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3899	3847	685	<800	9553	9383
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5672	5644	41	<800	166	<800
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1711	1683	388	<800	13615	13115
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862	854	2500	2497	4731	4632

	2368	2389	2889	2778	5159	5076
	-----	-----	-----	-----	-----	-----
	178	<800	4503	4430		
	-----	-----	-----	-----	-----	-----
	6589	6728	6607	6900		
	-----	-----	-----	-----	-----	-----
	3836	3895	2766	2803		
	-----	-----	-----	-----	-----	-----
Query Match 97.4%; Score 3492.8; DB 9; Length 197279;						
Best Local Similarity 99.4%; Pred. No. 0;						
Matches 3568; Conservative 0; Mismatches 12; Indels 8; Gaps 6;						
QY 1	GGATCCCTACCTTCCCATACAGCTAGAGGGGCGATGAGCGCTCCTGTAGATGAGGGA	60				
DB 186606	GGATCCCTACCTTCCCATACAGCTAGAGGGGCGATGAGCGCTCCTGTAGATGAGGGA	186665				
QY 61	CCCCAAGGAATGTCTCCCTGTGGGGCACTTCTTACAGATGGGATGGCCAGTGGTT	120				
DB 186666	CCCCAAGGAATGTCTCCCTGTGGGGCACTTCTTACAGATGGGATGGCCAGTGGCA	186725				
QY 121	AAGTTGGTGTGAGGCGAGAAAAAAGATCTAGTTTGTACTTGTAGAGTTTCCGGTTT	180				
DB 186726	AAGTTGGTGTGAGGCGAGAAAAAAGATCTAGTTTGTACTTGTAGAGTTTCCGGTTT	186785				
QY 181	GTTCAATGCGATGGGAGGAGCTCAAGAGACAGCAGCTTGGCTCAGTGGCTACAGTGCA	240				
DB 186786	GTTCAATGCGATGGGAGGAGCTCAAGAGACAGCAGCTTGGCTCAGTGGCTACAGTGCA	186845				
QY 241	GGAAAGGTGATATGCTTGGGCGAGGCGAGGCGCTGGTGAGGCGTATGTTAAACAG	300				
DB 186846	GGAAAGGTGATATGCTTGGGCGAGGCGAGGCGCTGGTGAGGCGTATGTTAAACAG	186905				
QY 301	GAGGCTCTCCATTTCCAGCCCAAGAGACGTAAGATGTAATCTTCATGATATATTAC	360				
DB 186906	GAGGCTCTCCATTTCCAGCCCAAGAGACGTAAGATGTAATCTTCATGATATATTAC	186965				
QY 361	TGCAAAACCCAGCAGAGGTTCCAGAAAAAGGCTGAGGTTGGAACCCAGTACCCCCAC	420				
DB 186966	TGCAAAACCCAGCAGAGGTTCCAGAAAAAGGCTGAGGTTGGAACCCAGTACCCCCAC	187025				
QY 421	TCAGAGACACCAAGTCAATATAATCAAGAGACCAAGAGACAGAACCCCTTCCCA	480				
DB 187026	TCAGAGACACCAAGTCAATATAATCAAGAGACCAAGAGACAGAACCCCTTCCCA	187085				
QY 481	CTCTGCCCATGTCTCAAGTTTACTGGCCCTTCTCCAGATCTCTGCCACCATCTTGA	540				
DB 187086	CTCTGCCCATGTCTCAAGTTTACTGGCCCTTCTCCAGATCTCTGCCACCATCTTGA	187145				
QY 541	AAGGAACACTGAAGAAGAACTGAAATTTAAGCTGACAGATTAAGAGGATGAGTAA	600				
DB 187146	AAGGAACACTGAAGAAGAACTGAAATTTAAGCTGACAGATTAAGAGGATGAGTAA	187205				
QY 601	ACCTAAATCATTTGTTCAATGATGATCAAGAGAAGTTTAAACACTTTGGACTAA	660				
DB 187206	ACCTAAATCATTTGTTCAATGATGATCAAGAGAAGTTTAAACACTTTGGACTAA	187265				
QY 661	TGTGTGAATCTTTTCTTCTGCTATCCAGACGATGAGAACTGTAAACAGACCAATA	720				
DB 187266	TGTGTGAATCTTTTCTTCTGCTATCCAGACGATGAGAACTGTAAACAGACCAATA	187325				
QY 721	GTTTGAGACTGAAGAATCATTTGACATTTGCTGATGATGATGATGATGATGATGAT	780				
DB 187326	GTTTGAGACTGAAGAATCATTTGACATTTGCTGATGATGATGATGATGATGATGAT	187385				
QY 781	GTTGACCTTAC-TTTGTAATCTTGCACACGGGCAATTCATATCTGCACAAGATAT	839				
DB 187386	GTTGACCTTAC-TTTGTAATCTTGCACACGGG---CATCCATATCTGCAC-AGAGATAT	187441				
QY 840	GTTAAACAGTGTAAATGCTGCATGAGAGATGGGTGATTTTACTTTTGCTTTGTC	899				
DB 187442	GTTAA-CAGTGTAAATGCTGCATGAGAGATGGGTGATTTTACTTTTGCTTTGTC	187500				

QY 900	TCTTCTTCTATTTGTTCTTACTTATTTACGATTAACCTATGTTTCCCAAAATGTAA	959
DB 187501	TCTTCTTCTATTTGTTCTTACTTATTTACGATTAACCTATGTTTCCCAAAATGTAA	187559
QY 960	AGGCATTTTGAAGCCTAATTCACAAACCTTCCACTATTTTGTATCTAAGTATGACCT	1019
DB 187560	AGGCATTTTGAAGCCTAATTCACAAACCTTCCACTATTTTGTATCTAAGTATGACCT	187619
QY 1020	GATTGAGACTGGGTAGACAGGTGAAGAACCAATACAGGTTTTTAAATTTTAAAT	1079
DB 187620	GATTGAGACTGGGTAGACAGGTGAAGAACCAATACAGGTTTTTAAATTTTAAAT	187679
QY 1080	TATTTATTTATTTATTTTATTTTGAAGAGTGTGCTGCGCCAGCGGTGAGTCA	1139
DB 187680	TATTTATTTATTTATTTTATTTTGAAGAGTGTGCTGCGCCAGCGGTGAGTCA	187739
QY 1140	GGGGGTGATCAGCTTCACTGACCTTCACCTTCATGAGGCTCAAGGATTTCTCCACT	1199
DB 187740	GGGGGTGATCAGCTTCACTGACCTTCACCTTCATGAGGCTCAAGGATTTCTCCACT	187799
QY 1200	CAGCCCCCAAGTATGTTGGGACACACGATATGCGCCACCATGCTGGCTAATTTCTAT	1259
DB 187800	CAGCCCCCAAGTATGTTGGGACACACGATATGCGCCACCATGCTGGCTAATTTCTAT	187859
QY 1260	TTTTTGTAGAGTATGAGATCTCATTTATTTGTCAGGCTGCTTAAATTTCTGGCTAG	1319
DB 187860	TTTTTGTAGAGTATGAGATCTCATTTATTTGTCAGGCTGCTTAAATTTCTGGCTAG	187919
QY 1320	GTAGACCTCCCACTGGGCGCTCCCAAGACTGAGGATTAACAGCATGAGCCAAAGTCCC	1379
DB 187920	GTAGACCTCCCACTGGGCGCTCCCAAGACTGAGGATTAACAGCATGAGCCAAAGTCCC	187979
QY 1380	TGCCATATGAGATTTTCTGCTGTGATCCATGACAGCTAGTAAATCAAGACTTGGCTGC	1439
DB 187980	TGCCATATGAGATTTTCTGCTGTGATCCATGACAGCTAGTAAATCAAGACTTGGCTGC	188039
QY 1440	TGACGTGGAGAGCTGCATGCTTCTTGAGGTGAGACTTGAAGCTGAAAGGCTCATAG	1499
DB 188040	TGACGTGGAGAGCTGCATGCTTCTTGAGGTGAGACTTGAAGCTGAAAGGCTCATAG	188099
QY 1500	GCAGCCCTGAAGCCCAAAACCAAAAGTTCTATGTTTATCATCTGATCATGTTGATTTT	1559
DB 188100	GCAGCCCTGAAGCCCAAAACCAAAAGTTCTATGTTTATCATCTGATCATGTTGATTTT	188159
QY 1560	ATGAAATTAACATGATTAATTAAGACACTACCTCAAACTGAGCAAACTTATGATATTT	1619
DB 188160	ATGAAATTAACATGATTAATTAAGACACTACCTCAAACTGAGCAAACTTATGATATTT	188219
QY 1620	TTTTTAAAGTTGACCTGTTTTTAAATCACTCTTGGAGAAAAAGAAATTAATACAAATA	1679
DB 188220	TTTTTAAAGTTGACCTGTTTTTAAATCACTCTTGGAGAAAAAGAAATTAATACAAATA	188279
QY 1680	ATTAAAGGTGAATPACAGGCTACTATACCTTGTCTCCAGATTAAGCAAGTTCTGTTCTT	1739
DB 188280	ATTAAAGGTGAATPACAGGCTACTATACCTTGTCTCCAGATTAAGCAAGTTCTGTTCTT	188339
QY 1740	TCTTCTTTAGATGCTGAAGTGCAGAGACACTGTGTGATTTGACGTGTGTAAGTCA	1799
DB 188340	TCTTCTTTAGATGCTGAAGTGCAGAGACACTGTGTGATTTGACGTGTGTAAGTCA	188399
QY 1800	AAATGTGATTTTTTTTCTCCACTGCTATGATGATGATGATGATGATGATGATGATG	1859
DB 188400	AAATGTGATTTTTTTTCTCCACTGCTATGATGATGATGATGATGATGATGATGATG	188459
QY 1860	CTGATGGAGCACACAAACCATTTGTTCTCAGTCTCATTTTCTCCTCAAAACCTGG	1919
DB 188460	CTGATGGAGCACACAAACCATTTGTTCTCAGTCTCATTTTCTCCTCAAAACCTGG	188519
QY 1920	AATGTGCAATTCATAGTGGAGATGTACCTTGACAGACCCATGAAAAAGATCAACAAG	1979
DB 188520	AATGTGCAATTCATAGTGGAGATGTACCTTGACAGACCCATGAAAAAGATCAACAAG	188579

QY 1980 TTCACCCAGGAGGCCCTATTTTCTATTTGAAATGCTTCTATTTGCTTC 2039
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Db 188580 TTCCACCCAGGAGGCCCTATTTTCTATTTGAAATGCTTCTATTTGCTTC 188639
QY 2040 TTTCATTTCTGCTCTCTACAGATTTCAGAGCTTTTCTGTTTCAATGGAAGCTCACAT 2099
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Db 188640 TTTCATTTCTGCTCTCTACAGATTTCAGAGCTTTTCTGTTTCAATGGAAGCTCACAT 188699
QY 2100 ACACCTCATTTTTTCTCTACACAAACCCCAAGTGAAGTGTCTCTCATTTGATATA 2159
| | | | |
Db 188700 ACACCTCATTTTTTCTCTACACAAACCCCAAGTGAAGTGTCTCTCATTTGATATA 188759
QY 2160 AGTAAGAGGAGCTCTGCTATTAGAGGCTTTGCCAGGACGAGCTGAGAGGCGCTAGAC 2219
| | | | |
Db 188760 AGTAAGAGGAGCTCTGCTATTAGAGGCTTTGCCAGGACGAGCTGAGAGGCGCTAGAC 188819
QY 2220 TGGCTCATTTTCATCTCATTTCTCATCTGACTTGTACCTGACCAAGCCCAACATGTGG 2279
| | | | |
Db 188820 TGGCTCATTTTCATCTCATTTCTCATCTGACTTGTACCTGACCAAGCCCAACATGTGG 188879
QY 2280 GCTCAGATTTGATCAATTTATTTTAAAGAGCAAAACATTTCCCGCATTTGGCCC 2339
| | | | |
Db 188880 GCTCAGATTTGATCAATTTATTTTAAAGAGCAAAACATTTCCCGCATTTGGCCC 188939
QY 2340 AGTTATTAGCATTTTCTCAGATTACCTTGAGAAATGCCATGCGCTGTATTTACAT 2399
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Db 188940 AGTTATTAGCATTTTCTCAGATTACCTTGAGAAATGCCATGCGCTGTATTTACAT 188999
QY 2400 CTTCACCTTTGCTCTCTCCCTCAGAAAGAGAAATGATGAGTGGCTCGAGAGAC 2459
| | | | |
Db 189000 CTTCACCTTTGCTCTCTCTCCTCAGAAAGAGAAATGATGAGTGGCTCGAGAGAC 189059
QY 2460 TAGTGATGCTTAACTGCTCTTCAATGATGCTGCTTATCTGTTTCTATTTTCTCC 2519
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Db 189060 TAGTGATGCTTAACTGCTCTTCAATGATGCTGCTTATCTGTTTCTATTTTCTCC 189119
QY 2520 TTTTCCACCGAAGTCTATATCTCAGAAAGAGAGCATGGCTTAAAGGCTCTGCT 2579
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Db 189120 TTTTCCACCGAAGTCTATATCTCAGAAAGAGAGCATGGCTTAAAGGCTCTGCT 189179
QY 2580 AAGAATATCAAGTCTCAGAGAAATCCCATTTGACTGAGCCCTCGTGTACCCCTTGT 2639
| | | | |
Db 189180 AAGAATATCAAGTCTCAGAGAAATCCCATTTGACTGAGCCCTCGTGTACCCCTTGT 189239
QY 2640 GATGAGAAAGCTCCAGAGGCTTGTCTTTTGCATTTTACAGGCTTAACTCAGACATCAC 2699
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Db 189240 GATGAGAAAGCTCCAGAGGCTTGTCTTTTGCATTTTACAGGCTTAACTCAGACATCAC 189299
QY 2700 AGGGGCAAGAAAGAAAGTAACCTAACTAATGCTGCTTATATTTGTAATTTGTAAT 2759
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Db 189360 AGTTAATTCAGTGTATGATGTATGATGTATGATGTATGATGTATGATGTATGATGTAT 189419
QY 2820 TGTGATTTGATTTATGCTATTTGGAATTAAGATGCTGTTAAGACACAGCCAGGTTTC 2879
| | | | |
Db 189420 TGTGATTTGATTTATGCTATTTGGAATTAAGATGCTGTTAAGACACAGCCAGGTTTC 189479
QY 2880 CTCAGTCCGCTGAGCAATTTTTCAAAGTTAAATTTAAATTTACATCTGAACTCTG 2939
| | | | |
Db 189480 CTCAGTCCGCTGAGCAATTTTTCAAAGTTAAATTTAAATTTACATCTGAACTCTG 189539
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Db 189540 TCACAGGAGAAATGACATGATGAGACTTAAAGATCTAGCCCAATTTTATTTACTT 189599
QY 3000 GTTAGAGGATTTTGAACAATTTACTAAATTTCTCAAGGTTCAATTTCCCATTAACAT 3059
| | | | |
Db 189600 GTTAGAGGATTTTGAACAATTTACTAAATTTCTCAAGGTTCAATTTCCCATTAACAT 189659
QY 3060 AATGAATGTCTCATCTTTTGGGGCCCTGGAGAGCATATTTACTGTAATGTATAAT 3119

Db 189660 AATGAATGTCTCATCTTTTGGGGCCCTGGAGAGCATATTTACTGTAATGTATAAT 189719
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QY 3120 CATTTGTTATTTATTTATATATTTTGTCTTTTAAATGATTAAGATTTTAAAGTAT 3179
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Db 189720 CATTTGTTATTTATTTATATATTTTGTCTTTTAAATGATTAAGATTTTAAAGTAT 189779
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QY 3180 GTAACTGTAAACATTAATAATGCAAAATGCGTAAGAGACAGTAAATATATGATTA 3239
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Db 189780 GTAACTGTAAACATTAATAATGCAAAATGCGTAAGAGACAGTAAATATATGATTA 189839
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QY 3240 TTATATTTGTTATTTATTTATTTAGCTTTTCTGTTGTTGTTATTTCTTTTAAATGC 3299
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Db 189840 TTATATTTGTTATTTATTTATTTAGCTTTTCTGTTGTTGTTATTTCTTTTAAATGC 189899
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QY 3300 TTAACAGAAATCTGTATCCCATTTCTTACACACACCCCAACATTTTGTGCTTTTCC 3359
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QY 3360 CATGCC-GGTCATGCTAACTTTGAAAGCTTCAGCTTTCTTCTTCAATCTTCTCG 3418
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Db 189960 CATGCCGGTCAATGCTAACTTTGAAAGCTTCAGCTTTCTTCTTCAATCTTCTCG 190019
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QY 3419 GCACCTGTATATGCTTTTGAATTCATGTTAAGATTCCTAGGCTGCTATCATGT 3478
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Db 190020 GCACCTGTATATGCTTTTGAATTCATGTTAAGATTCCTAGGCTGCTATCATGT 190079
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Db 190140 TTCAATTTGGGATTTGATTTTCTTCTTCTATACAGAGAGATGAA 190187
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RESULT 5
HSA312688 220965 bp DNA linear HTG 15-MAY-2002
LOCUS HSA312688
DEFINITION Homo sapiens chromosome 3 clone RP6-32g23 map 3p21.3, ***
ACCESSION AJ312688.2 GI:13559235
VERSION AJ312688.2
KEYWORDS HTG; HTGS_PHASE2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Kiss,H., Yang,Y., Kiss,C., Andersson,K., Klein,G., Imreh,S. and
Dumanski,J.P.
The transcriptional map of the common eliminated region 1 (C3ER1)
in 3p21.3
Eur J Hum. Genet. 10 (1), 52-61 (2002)
MEDLINE 21906202
PUBMED 11896456
REFERENCE 2 (bases 1 to 220965)
Kiss,H.
Direct Submission
Submitted (01-APR-2001) Kiss H., Microbiology and Tumorbiology
Center (MTC), Karolinska Institute, Box 280, Stockholm, S-17177,
SWEDEN
COMMENT
On Apr 5, 2001 this sequence version replaced gi:13548633.
The sequence is a consensus sequence of clone RP4-787c23 (1-140400
bp).
clone RP6-32g23 (31212-220965 bp), clone RP6-146e1 (partially,
1-6800 bp)
and clone RP6-188g11 (partially, 1-108303 bp). The sequencing
contigs are
in order and the gaps between them are represented by 100 Ns.
Contig 1:
1-11731 bp Contig 2: 11832-26218 bp Contig 3: 26319-28347 bp
Contig 4:

28448-42160 bp Contig 5: 42261-55059 bp Contig 6: 55160-61578 bp
Contig
7: 61679-97342 bp Contig 8: 97443-117655 bp Contig 9:
117556-118727 bp
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Contig 20: 191476-201473 bp Contig 21: 201574-202307 bp Contig
22:
202408-204878 bp Contig 23: 204979-213531 bp Contig 24:
213632-218109 bp
Contig 25: 218210-219800 bp Contig 26: 219901-220965 bp.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 26 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 11731: contig of 11731 bp in length
* 11732 11831: gap of 100 bp
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* 55160 61578: contig of 6419 bp in length
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VERSION AF224497.1
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AUTHORS Scotell,E.J.
TITLE CCR3 expression is associated with chromatin remodeling in Th2
cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 7010)
AUTHORS Scotell,E.J.
TITLE Direct Sublimation
JOURNAL Submitted (13-JAN-2000) Basel Institute for Immunology, 487
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LOCUS Homo sapiens CCR3 gene and exon 3.
DEFINITION AF237381
ACCESSION AF237381.1 GI:10643653
VERSION 1
KEYWORDS 2 of 2
SEGMENT Homo sapiens.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 3388)
AUTHORS Zimmermann,N., Daugherty,B.L., Kavanaugh,J.L., El-Awar,F.Y.,
Moulton,E.A. and Rothenberg,M.E.
TITLE Analysis of the CC chemokine receptor 3 gene reveals a complex 5'
exon organization, a functional role for untranslated exon 1, and a
broadly active promoter with eosinophil-selective elements
JOURNAL Blood 96 (7), 2346-2354 (2000)
MEDLINE 20458773
PUBMED 11001881
REFERENCE 2 (bases 1 to 3388)
AUTHORS Daugherty,B.L.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2000) Immunology & Rheumatology, Merck Research
Laboratories, 126 East Lincoln Avenue, Rahway, NJ 07065, USA
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VERSION	AX345239.1	GI:18493125			
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SOURCE					
ORGANISM					
REFERENCE	1				
AUTHORS	Olek A., Piepenbrock C. and Berlin K				
TITLE	Diagnosis of diseases associated with the immune system				
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ACCESSION	AX345238				
VERSION	AX345238.1	GI:18493124			
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE	1				
AUTHORS	Olek A., Piepenbrock C. and Berlin K.				
TITLE	Diagnosis of diseases associated with the immune system				
JOURNAL	Patent: WO 020928-A 309 03-JAN-2002;				
FEATURES	Epigenomics AG (DE)				
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OY	61	CCCCAAGGAATGTCCTCCCTGCGGGGCACTTCCTTACGAGATGGGATGGCCGCGGT	120		
DB	1514	TTTTTAAGGAATGTTTTTTTGT-GGGTATTTTTTTTATTTAGATGGGATGTTAGTGTAGTT	1572		
OY	121	AAGTTGGTGTCAGGCGAGAAAAAAGATCTAGTTGTACTCTTGAGATTCCTCGGTT	180		
DB	1573	AAGTTGGTGTCAGGCGAGAAAAAAGATTTAGTTGTATTTTGAAGATTTTCGGTT	1632		
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DB	1633	GTTTATGGATGGGAGGAGTCAAGAGTCAAGTATGTTTGTGTTTGTGTTTATTTAGTGA	1692		
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 VERSION AF262300.1 GI:19171642
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 REFERENCE
 1 (bases 1 to 1310)
 Vijn,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and

TITLE Michael,N.L.
Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
2 (bases 1 to 1310)
Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
REFERENCE Direct Submission
TITLE Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
JOURNAL Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA

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ACCESSION AF262304
VERSION AF262304.1 GI:19171650
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Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 436)
Vijh,S., Dayhoff,D.E., Wang,C.E., Imam,Z., Ehrenberg,P.K. and
Michael,N.L.
TITLE Transcription Regulation of Human Chemokine Receptor CCR3: Evidence
for a Rare TATA-less Promoter Structure Conserved between
Drosophila and Humans
JOURNAL Genomics 80 (1), 86-95 (2002)
MEDLINE 22074933
PUBMED 12079287
2 (bases 1 to 436)
Vijh,S., Dayhoff,D.E., Wang,C.E., Ehrenberg,P.K. and Michael,N.L.
REFERENCE Direct Submission
TITLE Submitted (23-MAR-2000) Dept. of Mol. Diag. and Pathogenesis,
JOURNAL Walter Reed Army Institute of Research, 1600 E. Gude Drive,
Rockville, MD 20850, USA
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repeat_region      8995. .9342
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repeat_region      9468. .9577
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repeat_region      12100. .12164
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repeat_region      12462. .12524
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misc_feature        12479. .13251
                    /note="CpG island (%GC=77.5, o/e=0.80, #CpGs=108)"
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misc_feature	13163..13207	/note="similar to	EST BF582271 (MID:g11655983)	"
repeat_region	14343..14554	/rpt_family="L2"		
repeat_region	15323..15417	/rpt_family="MIR"		
repeat_region	15528..15798	/rpt_family="L2"		
repeat_region	16310..16350	/rpt_family="L2"		
repeat_region	16655..16706	/rpt_family="MIR"		
repeat_region	16718..16837	/rpt_family="L2"		
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Query Match	6.1%;	Score 218.2;	DB 9;	Length 131329;
Best Local Similarity	74.3%;	Pred. No. 2.7e-38;		
Matches 289;	Conservative 0;	Mismatches 98;	Indels 2;	Gaps 1.

Qy	1012	TTCCACCTGTAATTAGACACTGGGAGTAGACAGGTGAAACCAATACAGATTTTTAATTTTTTAA	1071
Db	23473	TTAACACATTTTAAATTAATATGATTAATAATTTAAACATTAATTAATTAATTAATTAATTAATTT	23532
Qy	1072	TTTTTAATTAATTAATTAATTAATTAATTTTGAAGATGGAGTCCGG--CTGTGGCCAG	1129
Db	23553	TATTTATTTATTTATTTATTTATTTATTTATTTTGGAGACAGAGTCTCGCTCTGTACACCCAG	23592
Qy	1130	CTGAGATGCAGCGCGGTGATCAACAGTTCACCTGCAGCCCTCAACCTTCAAGGCTCAAGGGAT	1189
Db	23593	CTGAGATGCAAATGGTGTGATCAGACGATTACCTGCAGCCCTCCACCTCCTGGGTTCACAGAGAC	23652
Qy	1190	TCTCCACACTGCACACCCCAAGTAAGTTGGGACACACGATATGGCCACCATGCTGGCTTA	1249
Db	23653	TCTCTCTCCCTCACACCTCCCAAGTAGCTGGGATTAAGGCATGCACACCATGCTGGCTTA	23712
Qy	1250	ATTCTTATTTTGTGTGTAGAGATAGAGATGCATTAATGTGTGCAGGGGTGCTTGAATTC	1309
Db	23713	ATTTTTTGTATCTTTAAGTAGAGATGGGGTTTACCATGTGTGGCCACAGGCTGGTCTTGAACCTT	23772
Qy	1310	CTGGGCTCAGGTAGAGCTCCCACTGGGGCTCCCAAAATGACTGGGATTACAGGCATGAG	1369
Db	23773	CTGACCTCAGAGTAGTACACCTGCTCAGGCTCCCAAAAGTGTGGGATTACAGGCATGAGC	23833
Qy	1370	CAGAAGTCCCTGCCCATATGAGATTTTCT	1398
Db	23833	CACCGTGGCCAGCCCTCTTATATCTTCT	23861

RESULT 15	LOCUS	DEFINITION
HS50024/c	157335 bp	Linear
HS50024	Human DNA sequence from clone Rpi-50024 on chromosome 1p35.1-3p.3. Contains the 3' end of the gene for a novel protein similar to C. elegans K07B1.7 (Tr:001886), the gene for a novel protein (translation of CDNA NT82001100 (Em:AK001211)), the spf gene for stratiflin (14-3-3 protein sigma), the gene for a novel protein with DHHC zinc finger domain, the gene for a novel protein (translation of CDNA KAT07271 (Em:AK000484)) and the gene for B120 (clorf4) (ARID DNA binding domain containing protein). Contains ESTs, STSS, GSSs and six putative CPG islands, complete sequence.	PRI 17-MAY-2000

ACCESSION AL034380
VERSION AL034380.26 GI:7981257
KEYWORDS HTG: ARID; B120; Cpg island; DHHC; SFN; stratifin; zinc finger.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 157435)
AUTHORS Wilson, S.
TITLE Direct Submission
JOURNAL Submitted (19-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: hummerys@sanger.ac.uk
On May 22, 2000 this sequence version replaced gi:7228107.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/C.elegans/wormpep
This sequence was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Ch1
RPI-50024 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
VECTOR: pcypac2
This sequence is the entire insert of clone RPI-50024.
FEATURES
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/clone_lib="RPCI-1"
303..588
/note="AluX repeat: matches 1..294 of consensus"
684..989
/note="AluO repeat: matches 1..308 of consensus"
1188..1382
/note="MIR repeat: matches 42..241 of consensus"
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K07B1.7 (Tr:001886))"
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Em:T99610 Em:AA009447 Em:AA446768 Em:AT633701 Em:AI051662
Em:AT633702 Em:AT633712 Em:AW137695 Em:AA459367
Em:AA421592 Em:AI942463 Em:AI379622 Em:AW027151
Em:AA459592 Em:AW134811 Em:AW574517"
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/note="supported by EGENESH and GENSCAN
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/codon_start=1

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LGVHCKRPPRCOLKRRPRNGLGISTYDEPLPDQPTESLRRQPTSMKRTDMAP
VGGSCADSPEPLD"
2239..2408
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2415..2712
/note="AluSc repeat: matches 2..307 of consensus"
3200..3305
/note="MIR repeat: matches 47..171 of consensus"
3280..3330
/note="L2 repeat: matches 2577..2627 of consensus"
3965..4089
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4092..4225
/note="AluSc repeat: matches 3..137 of consensus"
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NT2RM2001100 (Em:AK001211)) (isoform 1))"
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Em:AA255975 Em:AA471875 Em:AT799690 Em:AT733568
Em:AT742159 Em:AT264192 Em:AA420443 Em:AA481285
Em:AI018507 Em:AA537066 Em:AT051243 Em:AA594566
Em:AT1224497 Em:AA255197 Em:AA420799 Em:AT141816
Em:AT129053 Em:AA932824 Em:AA417904 Em:AA120615 Em:W85966
Em:AT203699 Em:AA643378 Em:AT152186 Em:W23806 Em:AA437631
Em:AA427452 Em:AA437451 Em:AT1530536 Em:AA680497
Em:AT589175 Em:AT934607 Em:AT264710 Em:AA693180
Em:AT467417 Em:AA450558 Em:AA681360 Em:AT792158 Em:R02290"
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TSLATLWELDEPLHNLNLSKMDLEHNGKLAFNLDYATEVLDLSDYLDHLASDPFPHY
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6568..6688
/note="MIR repeat: matches 21..144 of consensus"
6650..6807

